

Title: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR

IMMUNE MODULATION

Applicant (s): Grant McFadden et al.

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FIGURE 1

TLKYCYTVTLKDNGLYDKVFYCHYN TPVgp38aa 1 MNKLILSLLGFVATCNCITLRYNYTVTVK-NGLYDGVFFDYYNDQLVTRI 49 Yabagp38

25 (8BQ ID NO: 1) TPVgp38aa 26 50 SYNHETKRGNVN 61 (SEQ ID NO: 2) Yabagp38



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FIGURE 2

YMTV partial gp38 gene (183 nucleotide):

5'
ATGAATAAGTTAATTTTATCGTTGTTGGGTTTTGTGGCAACTTGCAATTGTATAACCTTAAGATATAATTATACCGTTA
CGGTAAAGAATGGATTATACGACGGGGTATTTTTTGATTATTACAACGATCAGTTAGTAACGAGGATATCATAATCA
TGAAACCAAACGAGGAAATGTAAAT (SEQ ID NO: 3)

YMTV partial gp38 gene (61 amino acid):

MNKLILSLIGFVATCNCITLRYNYTVTVKNGLYDGVFFDYYNDQLVTRISYNHETKRGNVN (SEQ ID NO: 2)

MNKLILFSTIVAVCNCITLKYNYTVTLKDNGLYDGVFYDHYNDQLVTKISYNHETRHGNVNFRADWFKIS RSPHTPGNDYNFNFWYSLMKETLEEINKNDSTKTTSLSLITGCYETGLLFGSYGYVETANGPLARYHTGD KRFTKMTHKGFPKVGMLTVKNTLWKDVKTYLGGFEYMGCSLAILDYQKMAKGEIPKDTTPTVKVTGNELE DGNMTLECSVNSFYPPDVITKWIESEHFKGEYKYVNGRYYPEWGRKSDYEPGEPGFPWNIKKDKDANTYS LTDLVRTTSKMSSQLVCVVFHDTLEAQVYTCSEGCNGELYDHLYRKTEEGEGEEDEED*

FIG. 3

 SEQ ID NO: 5

Tana gp38:

AAGCTTCATGAATAAGTTAATATTATTTAGCACAATTGTAGCAGTTTGTAACT GCATAACTTTAAAATATAATTATACTGTTACGTTAAAAGATAATGGGTTATAC GATGGAGTATTITACGATCATTACAACGATCAGTTAGTAACGAAAATATCAT ATAACCACGAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGTTTAA TATTTCTAGGAGTCCCCACACGCCAGGTAACGATTACAACTTTAACTTTTGGT ATTCTTTAATGAAAGAAACTTTAGAAGAAATTAATAAAAACGATAGCACAAA AACTACTTCGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATTTG GTAGTTATGGGTATGTAGAAACGGCCAACGGACCGTTGGCCAGATACCATAC AGGAGATAAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCAAGGTTGGA ATGTTAACTGTAAAAAACACTCTTTGGAAAGATGTAAAAACTTATCTAGGCG GTTTTGAATACATGGGATGTTCATTAGCTATTTTAGATTACCAAAAAATGGCT AAAGGTGAAATACCAAAAGATACAACACCTACAGTGAAAGTAACGGGTAAT GAGTTAGAAGATGGTAACATGACTCTTGAATGCAGTGTAAATTCATTTTACCC TCCTGACGTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATAT AAATATGTTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCGATTATG AGCCAGGAGAGCCAGGTTTTCCATGGAATATTAAAAAAGATAAAGATGCAA ACACATATAGTTTAACAGATTTAGTACGTACAACATCAAAAATGAGTAGTCA ACTAGTATGTGTTTTTCCATGACACTTTAGAAGCGCAAGTTTATACTTGTT CTGAAGGATGCAATGGAGAGCTATACGACCACCTATATAGAAAAAACAGA AGAAGGAGAAGGTGAAGAGGATGAAGAAGACGGAAACCCTCGAG

MDKLLLFSTIVAVCNCITLKYNYTVTLKDDGLYDGVFYDHYNDQLVTKISYNHETRHGNVNFRADWFNIS RSPHTPGNDYNFNFWYSLMKETLEEINKNDSTKTTSLSLITGCYETGLLFGSYGYVETANGPLARYHTGD KRFTKMTHKGFPKVGMLTVKNTLWKDVKAYLGGFEYMGCSLAILDYQKMAKGKIPKDTTPTVKVTGNELE DGNMTLECTVNSFYPPDVITKWIESEHFKGEYKYVNGRYYPEWGRKSNYEPGEPGFPWNIKKDKDANTYS LTDLVRTTSKMSSQPVCVVFHDTLEAQVYTCSEGCNGELYDHLYRKTEEGEGEEDEED*

SEQ ID NO: 7

YLD gp38:

ATGGATAAGTTACTATTAGTTAGCACAATTGTAGCAGTTTGTAACTGCATAAC TTTAAAATATAATTATACTGTTACGTTAAAAGATGATGGGTTATACGATGGAG TATTTTACGATCATTACAACGATCAGTTAGTGACGAAAATATCATATAACCAT GAAACTAGACACGGAAACGTAAATTTTAGGGCTGATTGGTTTAATATTTCTA GGAGTCCCCACACGCCAGGTAACGATTATAACTTTAACTTTTGGTATTCTTTA ATGAAAGAAACTTTAGAAGAAATTAATAAAAACGATAGCACAAAAACTACTT CGCTTTCATTAATCACTGGGTGTTATGAAACAGGATTATTATTTGGTAGTTAT GGGTATGTAGAAACGGCCAACGGCCGTTGGCCAGATACCATACAGGAGAT AAAAGGTTTACGAAAATGACACATAAAGGTTTTCCCAAGGTTGGAATGTTAA CTGTAAAAAACACTCTTTGGAAAGATGTAAAAGCTTATTTAGGCGGTTTTGA ATATATGGGATGTTCATTAGCTATTTTAGATTACCAAAAAATGGCTAAAGGTA AAATACCAAAAGATACAACACCTACAGTGAAAGTAACGGGTAATGAGTTAG AAGATGGTAACATGACTCTTGAATGCACTGTAAATTCATTTTACCCTCCTGAC GTAATTACTAAGTGGATAGAAAGCGAACATTTTAAAGGTGAATATAAATATG TTAACGGAAGATACTATCCAGAATGGGGGAGAAAATCCAATTATGAGCCAGG AGAGCCAGGTTTTCCATGGAATATCAAAAAAGATAAAGATGCAAATACATAT AGTTTAACAGATTTAGTACGTACAACATCAAAAATGAGTAGTCAACCAGTAT GTGTTGTTTTCCATGACACTTTAGAAGCGCAAGTTTATACTTGTTCTGAAGGA TGCAATGGAGAGCTATACGATCACCTATATAGAAAAACAGAAGAAGGG GAAGGTGAAGAGGATGAAGAAGACTGA

MITKAIVILSIITAYVDASAFLVYNYTYTLQDDNHRYDFEVTDYFNDILIKRLKLNSETGRPELRNEPPT WFNETKIRYYPKNNYNFMFWLNRMSETLDEINKLPETSNPYKTMSLTIGCTDLRQLQVNFGYVTVGGNIW TRFDPKNKRFSKVRSRTFPKVGMLTVKSQHWERVMEHLGSMVTLTCPFTADDYYKISKGYIDKPVKPTVT VTGIERGDNTTLICTFDNHYPSSVAVKWYNIEDFAPDYRYDPYVNELLPDTDYLPGEPGYPTITRRLGDK YLFTSSPRVMVPTIMSNRIACVGFHSTLEPSIYRCVNCSGPEPVLQYQGDRRNDLEDEED

SEQ ID NO: 9

Swinepox C1L

ATGATTACTAAAGCGATTGTGATATTGTCTATTATTACAGCATATGTAGATGC TTCCGCATTCTTAGTATACAATTATACATATACTTTACAAGATGATAATCATC GATATGACTTCGAAGTCACCGATTATTTTAATGATATACTAATAAAACGTTTA AAACTAAATAGCGAGACAGGAAGACCAGAATTAAGAAATGAACCACCAACA TGGTTTAATGAGACTAAGATTAGATATTATCCGAAAAATAATTATAATTTTAT GAAACGAGTAATCCTTACAAGACTATGTCCTTGACAATTGGATGTACTGATCT AAGACAACTTCAAGTAAATTTCGGTTATGTTACTGTAGGTGGTAATATATGGA CACGATTCGACCCCAAGAATAAACGCTTTAGTAAAGTTAGATCACGTACATT TCCAAAGGTAGGAATGTTAACTGTTAAATCACAACACTGGGAACGTGTTATG GAACATCTTGGATCAATGGTAACATTAACATGTCCGTTTACAGCGGATGATTA TTATAAAATTTCTAAGGGATATATAGATAAGCCAGTTAAGCCTACTGTTACAG TTACAGGAATTGAAAGAGGAGATAATACTACATTGATATGCACATTTGATAA TCATTATCCGTCGTCGCTGTTAAATGGTATAACATCGAGGACTTTGCTC CGGACTATCGTTATGATCCGTACGTAAATGAATTGCTTCCTGATACGGACTAT CTACCGGGTGAACCAGGATATCCGACTATAACTAGGAGATTAGGTGATAAAT ATTTATTTACATCATCACCTAGGGTTATGGTACCAACTATCATGTCTAATAGA ATAGCATGTTGGATTTCATAGTACGTTAGAACCAAGCATATATAGATGTGT AAACTGCTCGGGACCTGAGCCTGTTTTACAATACCAGGGAGAT AGAAGGAATGACTTGGAGGATGAGGAGGATTAA

ClustalW Formatted Alignments

SYNHET.	120 S L S L 1 T G C S L S L 1 T G C S L S L 1 T G C T M S L T 1 G C	180 DVKTVLGG DVKAVLGG TVKKYVGG	240 P D V T K W P D V T K W P D V K W S S V A V K W Y	8 T T S K M S S R T T S K M S S R T T S K M S S N M S S N M S S N M V P T I M S N W V P T I M S N	<i>098</i>
50 N D Q L V T K N D Q L V T K N D Q L V T K N D Q L V T K	ND ST KT T ND ST KT T ND ST KT T E E SD KC S	170 VKNTLWK VHGPSWQ	SONSEYP SVNSFYP NVNSFYP TFDNHYP	230 YSLTDLV YSLTDLV YSLTDFG FTSSPRV	95 Q Q Q Q
40 K V F Y D H Y G V F Y D H Y G V F Y D Y Y F E V T D Y Y	EENN. KEENN. KEE	PKVGMLT PKVGMLT PKVGMLT PKVGMLT	ZZO G NM T L E C G NM T L E C G NT T L K C	280 KDKDANT KDKDANT KDGGKTT	340 8 1 Q E E E E E E E E E E E E E E E E E E
DN GE YD DN GE YD DD GE YD NN GE YD DD NHRYD	S LMKET L S LMKET L P LM KDT L N RMS BT L	KMTHKGF KMTHKGF KMTDKGF KVRTDRGF	TGNELED TGNELED TGEELQD	GFPWNIK GFPWNIK GFPLHPK GYPTITR	R K T E E G
30 NYTVILK NYTVILK NYTVILK NYTVILK	WANAMAYAYAYAYAYAYAYAYAYAYAYAYAYAYAYAYAYAY	150 KR FTTT G D KR FTTT G D KR FTTT T K N KR FTTT F K N KR FTT F K N KR FTTT F K N KR FTT F K N K N K F K N K K FTT F K N K K FTT F K N K K F K N K K F K N K K F K N K K F K N K	210 T T P T V K V V M P T V T V V M P T V T V	270 FEPCEP OVEPCEP OVEPCEP	330 330 330 330 330 330 330 330
20 11 L K V 1 . C 1 T L K V 1 . C 1 T L K V V 1 . C 1 T L K V V V V V V V V V V V V V V V V V V	SPHTPGND SPHTPGND SPHTPGDD SPHTPGDD	140 GPLARYH GPLARYH GPLARYS INIWTRED	ZOO K K G E I P K D K K N N N I P S N K G Y I D K P	260 PEWGRKS PEWGRKS PEWGRKS PEWGRKS	320 C S B G C N G C S B G C C B G C S B G C C B G
TI VAVCN G F VAVCN G F VAVCN G F VAVCN	WF K I S R W F D I S R W F N E I S R	GYVETAN GYVETAN GYVESSO	L D Y Q K M A F D Y Q K M A F D Y Q K M A	Y Y N G R Y Y Y Y N G R R Y Y V N G R E Y Y D P · · · Y V	LEACVYTERSIONT
70 M N K L 1 L F S M D K L L L F S N K L I L S L L T K A I V I L S	GNVNFRAD GNVNFRAD GNVNSRAS ELRNBPPT	130 T G L L F G S Y T G L L F G S Y T G L L P G S Y	YMGCSLAI YMGCSLAI YAGCSLAI TLTCP FTA	Z50 EHFKGEVK KYFNGEVK KYFNGEVR EDFAP	370 V C V V F H D T V C V V F H D T V C V V F H D T A C V O F H D T
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IPV go38 2600 (pepilde) IPV go38 YLDV gp38 YMTV gp38 SPV_C1L	TPV ga38 2soa (peptide) TPV ga38 YLDV ga38 YMTV ga38 SPV_C1L	IPV gp38 2600 (peptide) IPV gp38 YLDV gp38 WITV gp38 SPV_C11	TPV gp38 2600 (peptide) TPV gp38 YLDV gp38 YMTV gp38 SPV_C1L	TPV gp38 2600 (peptide) TPV gp38 YLDV gp38 YMTV gp38 SPV_C IL	IPV ga38 26aa (peptide) IPV ga38 YLDV ga38 YMTV ga38 SPV_C11